


```

FT      misc_feature          5941..6000                /tag= d
FM                                             /note= "these bases represent a line of missing text in
PT                                         the sequence listing in the specification. They
PT are included to maintain the nucleotide numbering
PT given in the specification for this DNA sequence"
EM      misc_feature          7741..7800                /tag= e
FM                                             /note= "these bases represent a line of missing text in
PT                                         the sequence listing in the specification. They
PT are included to maintain the nucleotide numbering
PT given in the specification for this DNA sequence"
EM      EP786519-AZ.
PM      30-JUL-1997.
PD
XX      07-JAN-1997;    97EP-010017.
PE
XX      05-JAN-1996;    96US-0009861.
PR
XX      (HUMA-) HUMAN GENOME SCT INC.
PA      Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA;
PI      Rosen CA;
XX      WPI: 1997-374922/35.
DR
XX      Polynucleotide(s) and proteins derived from Staphylococcus aureus -
P1 stored on computer readable medium and used in the production of
P1 anti-S.aureus vaccines
PS
XX      Claim 1; Page 729-734; 3271pp; English.
SX
XX      This sequence represents one of 5191 Staphylococcus aureus DNA sequences
CC of the invention. The DNA sequences are recorded on a computer readable
CC medium, preferably selected from a floppy or hard disk, random access
CC memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using
CC the S.aureus DNA sequences allows putative functions to be assigned so
CC that protein-encoding or regulatory regions of commercial, therapeutic or
CC industrial importance can be obtained. Specifically, sequences which are
CC likely to encode antigens have been identified and these polypeptides can
CC be used in a vaccine composition against S.aureus infection. The
CC polypeptides can also be used in a kit for the immunodetection of
CC S.aureus in a sample. S.aureus is implicated in numerous human diseases,
CC including cellulitis, eyelid infections, food poisoning, osteomyelitis,
CC skin and surgical wound infections, scalded skin syndrome, toxic shock
CC syndrome, etc. Organisms transformed with the DNA sequences can be used
CC for recombinant production of the polypeptides. The new DNA sequences
CC (and their fragments) are useful as primers or probes for isolating
CC homologues of any of the S.aureus DNA sequences contained on the
CC computer readable medium.
SC
XX      Sequence 7900 BP; 2600 A; 1138 C; 1511 G; 2348 T; 303 other;
SY
YY      Query Match          6.1%; Score 131.6; DB 18; Length 7900;
YY      Best Local Similarity 43.3%; Pred. No. 3.5e-31;
YY      Matches 714; Conservative 0; Mismatches 914; Indels 20; Gaps
OY      345 gaacatlaattgacacttggaagctcaagggtggaaaggcagttaigtgttggttg 404
Db      1589 gaaagcatatgataaacgcattacaagaacgatggagatatagatcacttgttatgccaga 1648
OY      405 gagagccctaaccgatcgctgatatcgtlccgcgaalccagata-----ttgagtggttc 459
Db      1649 gacctaatcgccgatcgatcgatgttacgtaacgagtggagaaatcaatlaattattcac 1708
OY      460 acgttcgaatatgagggaagcgcgcgctttgcagccgcgtgcccgaatcgttgatcactgagg 519
Db      1709 atgtacgcatcaggaagaatagcaaacttagcgcgctgcctgtttaaccaaaaattaactqta 1768

```

QY	520	agctgacgaatctgctgctctctgctgctctctggaacacacacccgcttaacggctctt	579
Db	1769	aaatcgtgtgcatctaaagtaatctggtgcccctggttaattactttatnaatgtaatg	1820
QY	580	atgattcgcacgaatgctgcgaaggctgttgcacgcgtgaacatctccgaagccc	639
Db	1829	atgattgcacaaatgataatgttaaccgaatatatattctgcacaaacgaatgatacg	1888
QY	640	agattggttcgaagctctctccgaagaaacgcaccccgagatcttgtttaagaaatgcctg	699
Db	1889	cacttgcgaacgaagcatctccgaagaacaaatttcaaaaattatgtgaagtgtgacgg	1946
QY	700	gttactgcgaatgtgtgaatggtgtgaagcgtgtaacgcatttttgataccgcgattc	759
Db	1949	tttaatacaccaaaattgaaanaagtgacaaatgttttgaataacggttaacgaagcaatc	2008
QY	760	agtcaccatcgtcgggttaaaggtgtgcggtgtgtgattccctgtgtatccgtaacg	819
Db	2009	gtacggcctatgaaacaaaaggtgtgctgtttatttgccttaacgcattataactg	2066
QY	820	aagacgcaggtgacggtactattccaatccatacttctctgcgaacctgcgtgtgt	879
Db	2069	aaaa---aattaaagatacaacgaataaacgtagatgatacatgaagacacagtagtat	2122
QY	880	tcccggaatccactcagaaagcgtgcagcgtgtgtgaagcggattacaacgcgtaaatcgtgca	939
Db	2126	caccaaaatacaaaagacatcaaaaagcgggttaaatatataataaagaataaaagcgtg	2185
QY	940	cttggttcgtgcgtgcggcggtgtgaagatctccgcgcgaaggtgtgtgaggtgtgcgagga	999
Db	2186	tcatgttaattggtgtagtggtgcgaanaatgcgaagaatgtagcttaacgttgattattgaa	2245
QY	1000	agattaaatcacgaatcgggcattgcgtgtgtgtgaagagataccacgcacgtgaacatc	1059
Db	2246	tgcctaataatccgttcatcattcatcattacagactaaacaatcttgcggatgctatc	2305
QY	1060	cgtttgaggtcgtgcattgtctgcgcctgtgtgttaagcggccgtgcgtgtgatagtccaatg	1119
Db	2306	catatagatcatgttaactcttggtgaanaatcgtaacnnnnnnnnnnnnnnnnnnnnnnnn	2365
QY	1120	agcgcatcgtctatctctatctgtgtacgagatctccctatctctatctctcctctaag	1179
Db	2366	nn	2425
QY	1180	acaaacgttgcaccaggtgtgatatacaacggtgtgcacattgtgtgcaggttacacgcgtgaagt	1239
Db	2426	aaaatttaaagccatccaattgaca-----caatccataaatatgcgacatgctt	2479
QY	1240	atccggtgacccggtgattgtgtgcgaacaacatcgaataattttgcctcatgtgtgaagaaa	1299
Db	2480	tcaataataatgttagaagaattgtgtgcgaatgataaattgcgttttgatacgaattaaactgaaa	2539
QY	1300	aaacacagctgttccctccttgatccgatact---caagcacacagcgcgtgaagtgtgagct	1356
Db	2540	atatataacatgttgcctgaagaagccatttcaacaaaacglttaagaactgaagcggcttt	2599
QY	1357	cggtgtgtagagacgttacacacaaacgltcgcgaagcattgtgcctatccaacctgatacag	1416
Db	2600	gggataaatgtatgtgaacaagaataaaaataatataatgtaaaccaattacgtccagaagat	2659
QY	1417	ttgcctctattttgaaacgagcgtgcggataaagatgacggttttactgtgtataccgcga	1476
Db	2660	taatgtgatacaatcaataaatttatataagaatgtatgcagtgtattccagaaatgtatgta	2719
QY	1477	tgtgtcaatgtgtgcacgtgcgaagtatacatcgaataatccgaggaagcgcgcgaacttggg	1536
Db	2720	cagcaacaagtttgcataactcgatactt---aaactgtgttaataacaagttcacca	2776
QY	1537	gttcatctccgcacgcacgataatgtgtcaaatgtcgttgcctcatcgaattgtgtgcgaaggt	1596
Db	2777	tttcaagtgttgatgttaacaatgtgtgtgcgttccctccaggtgcacattgcatcaaaaattg	2836
QY	1597	ttgatcgaaaacgcgcaggtgtatctgcgagatgtgtgtgcgaatgtgtgttggcagatcgtcgtcg	1656

DB	Accession	Organism	Gene	Protein	Function	Reference
DB	403	<i>gallitactyltaeaeagccgicacatgctgcacacgttgcacacatgttatatgacgaagcaatc</i>	462			
Oy	759	<i>cagtcaccacatgctgcgggataaagctgctgcgttgtagtattccctggtatcgcctaag</i>	818			
Db	463	<i>cgacgcgcctacgcgcacacaaagctgctgctgttgtaaatccacagtcattacatg</i>	522			
Oy	819	<i>gaaga</i>	823			
Db	523	<i>caaca</i>	527			
RESULT	5					
TI2801						
ID	TI2801	standard; DNA; 2841 BP.				
XX	TI2801;					
XX	08-OCT-1996	(first entry)				
DE	E. coli livGMEDA operon.					
XX						
KW	livGMEDA operon; modification; livG; livM; livE; livD; livA;					
KW	threonine deaminase; L-valine; L-isoleucine; L-leucine; repression;					
KW	transformation; bacterial host; lipolic acid; H+-ATPase deficient;					
KW	production; high yield; ds.					
XX						
OS	<i>Escherichia coli</i> .					
XX						
FH	Key	Location/Qualifiers				
FT	CDS	957..1055				
FT		/*tag= a				
FT	CDS	1195..2841				
FT		/*tag= b				
FT	attenuator	1081..1104				
FT		/*tag= c				
FT	misc_feature	52..57				
FT		/*tag= d				
FT	misc_feature	2395..2400				
FT		/*tag= e				
FT		/note= "KpnI cleavage site"				
XX						
PN	M09606926-A1.					
PD	07-MAR-1996.					
XX						
PP	30-AUG-1995;	95MO-JP01719.				
XX						
PR	30-AUG-1994;	94JP-0204856.				
XX						
PA	(AJIN) AJINOMOTO CO INC.					
XX						
PI	Hashiguchi K, Ishigooka M, Kurehashi O, Tomita F;					
PI	Yokota A;					
XX						
XX	WPI: 1996-160357/16.					
DR	P-PSDB: W02200, R88842.					
XX						
PT	Efficient microbial prodn. of L-valine and L-leucine - by culturing					
PT	<i>Escherichia coli</i> strain which requires lipolic acid for growth and/or is					
PT	deficient in H+-ATPase					
XX						
XX	Claim 8; Pages 31-36; 53pp; Japanese.					
XX						
CC	The present sequence is the E. coli livGMEDA operon, which can be					
CC	modified by the removal of nucleotides 953-1160 to express only					
CC	the livG, livM, livE and livD genes, but not the livA (threonine					
CC	deaminase) gene, which is required for L-valine, L-isoleucine					
CC	and/or L-leucine repression. The modified operon can be used to					
CC	transform a bacterial host, esp. E. coli, which requires lipolic					
CC	acid for growth and/or is deficient in H+-ATPase, for the efficient					
CC	prodn. of L-valine and L-leucine in high yield. A specific example					
CC	is the transformed H+-ATPase deficient E. coli strain					

CC W1485ctpA401/pmmdAR6, which when cultured in 1 microg/L lipolic acid
CC at 37 degrees C for 24 hrs. gave 8.0 g/L L-valine in the medium,
CC compared to 0.1 g/L for the untransformed strain.
XX
S0 Sequence 28A1 BP; 692 A; 707 C; 734 G; 708 T; 0 other;

Query Match	2.88;	Score 60.8;	DB 17;	Length 2841;
Best Local Similarity	45.88;	Pred. No. 7.8e-09;		
Matches 209;	Conservative 0;	Mismatches 247;	Indels 0;	Gaps 0;

QY	341	cgcaaacacaatlaatttgcacatttgcgaagctcaaaagcttgtaagcgcaatttcaagttgct	400
Db	1203	cgcaaacagtggttgtaacatctgcttgcggcgcaaaaggttgtaaacaccgcttccgttatcc	1262
QY	401	gggtgacagccttaattccgatactgagatgctgtccgcgaatcagatatgtgaattgggtgca	460
Db	1263	gggttgcgcaattatgaccggtttacgcattgttatgtacggtcggtgaggaacttgct	1322
QY	461	cgcttgaatatgaggaagcggtcggtcttgcagccggttcgcgaatcgtttgatactgggga	520
Db	1333	atgcgcgacatgagcagggctgcggcaatgycggtactatcgattatgctcgttaccggca	1382
QY	521	gctggcagatctgctgtcttcttgctgtccttgaaacacacacacctgattcaggtctta	580
Db	1383	aactgscgtatgtatcgcgaacgctgcgtccggcgcgcaaacacacctgataccgggtctgc	1442
QY	561	tgattcgacatcgaaatgctgtgcgaaggctgttgcatactgatacatatccgagtgcga	640
Db	1443	ggacgcactgtttagatttccatccctgtgtgtccataccggctcaagtgctccgcaccgt	1502
QY	641	gattgttcctgcagcgtctcttccagaagaacgcatcccgagatttgcgttcaaggaaatgcctcg	700
Db	1503	tatcggcaactgaacgcatcttcagaaagtgaatgtccctggatgtgctgttagcctgtacaa	1562
QY	701	ttaactgcagagatgctgtaactgtgtgcgaacaggttgaaacgatttgcatacgcgattca	760
Db	1563	gcatagcttcttcgtgcgacgctgcgtgaaagagtgtgcgcgcatacatcgtcgaagcaatcga	1622
QY	761	gtccacccatgvcggttaaggtgtctcgtcgtgtgta	796
Db	1623	cgttgcctgcataagctgcctcgtgcggttctgt	1658

RESULT 6

ID	T07115	T07115 standard; DNA; 2841 BP.
AC	T07115;	
XX	15-Oct-1996	(first entry)
DE	E. coli thrABC operon. and ilvGMEGA operon-containing DNA sequence.	
XX	thrABC operon: ilvGMEGA operon; thrA gene; ilvA gene; amino acid:	
KW	aspartokinase-I; homoserine-dehydrogenase-I; threonine-deaminase;	
KW	enzyme; metabolic engineering; L-isoleucine; feedback inhibition; ds.	
OS	Escherichia coli.	
XX		
XX	Key	Location/Qualifiers
FT	CDS	957..1052
FT		/*tag= a
FT		label= thrABC operon
FT	CDS	1195..2838
FT		/*tag= b
FT		label= ilvGMEGA operon
FT	attenuator	1081..1104
FT		/*tag= c
XX		
PN	EP685555-A1.	
XX		
PD	06-DEC-1995.	

XX 30-MAY-1995; 95EP-0108315.
 XX
 XX 30-MAY-1994; 94JP-0116340.
 XX
 XX (AJIN) AJINOMOTO CO INC.
 XX Hashiguchi K, Kishino H, Matsui H, Tsujimoto N;
 PI WPI; 1996-012380/02.
 DR P-PSDB; R66880, R66881.
 XX
 PT New Escherichia transformant producing L-isoleucine - carrying thr
 PT ABC operon, ilvGMDA operon and Opt. Lys C gene, all of which are
 PT released from feedback inhibition
 XX
 PS Claim 4; Page 35-38; 48pp; English.
 XX
 CC This sequence is present in E. coli and encodes a thrABC operon
 CC which comprises a thrA gene coding for aspartokinase-I-threonine-
 CC dehydrogenase-I which is released from inhibition by L-threonine, and
 CC an ilvGMDA operon which comprises an ilvA gene coding for
 CC threonine-deaminase which is also released from inhibition by L-
 CC isoleucine and which has its region required for attenuation removed.
 CC More specifically, base 953 to 1160 in which resides the attenuator
 CC sequence is deleted. The novel bacterium containing this sequence,
 CC E. coli AJ12919, may be used to produce L-isoleucine.
 XX
 SQ Sequence 2841 BP; 692 A; 706 C; 735 G; 708 T; 0 other;

Query Match 2.8%; Score 60.8; DB 17; Length 2841;
 Best Local Similarity 45.8%; Pred. No. 7.8e-09;
 Matches 209; Conservative 0; Mismatches 247; Indels 0; Gaps 0;

OY 341 cgcgaacaataattgacactttggaagctcaagtgatgaagcaatttatgtgtt 400
 DB 1203 cgcgaagtggtggtacatcggttcgagcagaagtgatgaacacggtttcggtatcc 1262
 OY 401 ggtgacagccttaacatcgatcgatgacgtgctgcacacatgatattggtgtgca 460
 DB 1263 ggtgacagccttaacatcgatcgatgacgtgctgcacacatgatattggtgtgca 460
 OY 461 cgttcgaatgagaagcgagcggtttgcagcggtgcgaatcgttgcactgagga 520
 DB 1333 atgcgacatgagcgaggttcgcaatgagcggtatgctgtatgctgtacccgcaa 1382
 OY 521 gctgcagatggtgtgtcttctgtgtgtcctggaacacacacccggtatcaggtctta 580
 DB 1383 aactgagctatgatacgcaacgctgtcgcgagcgcaacacacccggtatcaggtctta 580
 OY 581 tgatcgatcgaaatggtgcaaggtgttcgacgctgcacacacacccggtatcaggtctta 640
 DB 1443 gtagcagcactgttagatccatccctgtgtgtgcacacacccggtatcaggtctta 1502
 OY 641 gattgttcgacgttcttcacaggaacgacacccggtatggttttaaggaatgctctg 700
 DB 1503 tatcgacatcgac 1562
 OY 701 ttacgcaagatggtggaatggtggtgagcaggtggaagcatttggcctacgacatca 760
 DB 1563 gcatagcttctgtgtgacgtgcgtggaagatggtgcgacacatgctcgaagcattga 1622
 OY 761 gtcaacacatgaggtggtggtggtggtggtggtggtggtggtggtggtggtggtg 796
 DB 1623 cgttgcctgcacaggtgcctgcctgcctgcctgcctgcctgcctgcctgcctgcct 1658

RESULT 7
 T62750
 ID T62750 standard; DNA; 2841 BP.
 XX
 AC T62750;

XX 14-NOV-1997 (first entry)
 DT
 XX Escherichia coli ilvG gene.
 DE
 XX ilvG; L-isoleucine; production; ds.
 KW
 XX Escherichia coli.
 OS
 XX
 FH Key location/qualifiers
 FT CDS 957..1055
 FT /tag= a
 FT /product= W13730
 FT attenuator 1081..1104
 FT /tag= b
 FT CDS 1195..2841
 FT /tag= c
 FT /product= W13731
 FT misc_feature 52..57
 FT /tag= d
 FT /label= cleavage_site(SmaI)
 FT misc_feature 2395..2400
 FT /tag= e
 FT /label= cleavage_site(KpnI)

W09708333-A1.

06-MAR-1997.

27-AUG-1996; 96WO-JP02399.

30-JUL-1996; 96JP-0200860.

30-AUG-1995; 95JP-0221561.

(AJIN) AJINOMOTO CO INC.

Ito H, Izui M, Kishino H, Kurahashi O, Ono Y;

WPI; 1997-179289/16.

P-PSDB; W13730, W13731.

Production of L-amino acids (phenylalanine etc) by microbial culture
 PT - using microorganisms such as Escherichia or Corynebacterium having
 PT an enhanced ability to produce phosphoenolpyruvic acid
 XX
 PS Example 5; Pages 26-31; 41pp; Japanese.
 XX
 CC The present sequence is the Escherichia coli ilvG gene, which is
 CC involved in the production of L-isoleucine.
 CC
 XX

Sequence 2841 BP; 692 A; 706 C; 735 G; 708 T; 0 other;

Query Match 2.8%; Score 60.8; DB 18; Length 2841;
 Best Local Similarity 45.8%; Pred. No. 7.8e-09;
 Matches 209; Conservative 0; Mismatches 247; Indels 0; Gaps 0;

OY 341 cgcgaacaataattgacactttggaagctcaagtgatgaagcaatttatgtgtt 400
 DB 1203 cgcgaagtggtggtacatcggttcgagcagaagtgatgaacacggtttcggtatcc 1262
 OY 401 ggtgacagccttaacatcgatcgatgacgtgctgcacacatgatattggtgtgca 460
 DB 1263 ggtgacagccttaacatcgatcgatgacgtgctgcacacatgatattggtgtgca 460
 OY 461 cgttcgaatgagaagcgagcggtttgcagcggtgcgaatcgttgcactgagga 520
 DB 1333 atgcgacatgagcgaggttcgcaatgagcggtatgctgtatgctgtacccgcaa 1382
 OY 521 gctgcagatggtgtgtcttctgtgtgtcctggaacacacacccggtatcaggtctta 580
 DB 1383 aactgagctatgatacgcaacgctgtcgcgagcgcaacacacccggtatcaggtctta 1442

DR WPI: 1998-272225/24.
XX
PT Computer-readable medium with recorded Streptococcus pneumoniae
PT polynucleotide sequences - useful in diagnostic kits and assays, and
PT pharmaceutical compositions and vaccines for Streptococcus
PT pneumoniae
PS
PS Claim 1; Page 431-445; 1409pp; English.
XX
XX The present invention describes a computer readable medium which has
CC the nucleotide sequences SEQ ID NO:1 to 391 (V52134 to V52524) recorded
CC on it, or a representative fragment or a sequence at least 95% identical
CC to SEQ ID NO:1 to 391. The nucleotide sequences depicted in SEQ ID NO:1
CC to 391 (V52134 to V52524) are genomic fragments from Streptococcus
CC pneumoniae. The present invention also describes an isolated nucleic acid
CC molecule encoding a homologue of any of the fragments of the S. pneumoniae
CC genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced
CC by a process comprising: (a) screening a genomic DNA library using as a
CC probe a target sequence defined by any of the sequences in SEQ ID NO:1
CC to 391, identifying members of the library which contain sequences
CC that hybridize to the target sequence and isolating the nucleic acid
CC molecules from the members; or (b) isolating mRNA, DNA or cDNA produced
CC from an organism, amplifying nucleic acid molecules whose nucleotide
CC sequence is homologous to amplification primers derived from the
CC fragment of the S. pneumoniae genome to prime the amplification and
CC isolating the amplified sequences. The computer readable medium can be
CC used in a computer-based system for identifying fragments of the
CC S. pneumoniae genome of commercial importance, or expression modulating
CC fragments of the S. pneumoniae genome. Products from the present
CC invention can be used in diagnosis kits and assays, and pharmaceutical
CC compositions and vaccines for S. pneumoniae.
XX
SQ Sequence 25002 BP; 7422 A; 5498 C; 4618 G; 7463 T; 1 other;
Query Match 2.8%; Score 59.8; DB 19; Length 25002;
Best Local Similarity 46.2%; Pred. NO. 6e-08;
Matches 236; Conservative 0; Mismatches 272; Indels 3; Gaps 1;
XX
343 cagaacaattatgacacttggaaagctcaagtgatgaagcgaattatgtgtgctg 402
DB 6437 CTGACGCAATGCTTAACTATTGAAACATGCGGCGTAGATACATCTACGATCCCAT 6378
XX
403 gtgacagccctaatacgcgactgctgtccgcaaa---tcagatatgaagtgatgac 459
DB 6377 CAGGAACCTCAGCTCATCTTGAATGACGCTTGGCTGAGACAAAGATATCCGTTCTTAC 6318
XX
460 acgttcgaatgaaggaagcgcgcgttgcacgcgcgtgacgaatcgttgatcactggg 519
DB 6317 AAGTTCCGCGACGAAAGACAGAGTGTCTTGGACGCGTTATGCAACGTAATTCGGCGCT 6258
XX
520 agctgcagatgctgtctctctgtgtgtcgtgaacacacacactgtgttcagtcctt 579
DB 6257 CAATCGGGGTTGCACTTGTGATGAGTGTGACAGTGCACATCATTGATTAAGGTTT 6198
XX
580 atgattcgatcgaagaatggtgcaagtggttgccatgcgtacgcatatcccgatgccc 639
DB 6197 ACGATGACGACTATGATTAACACTCCATTCCTAGCGATCTTGATCAGCTCAAGTTAAG 6138
XX
640 agattggttcgacgtctctccaggaacgcacatccggaatttggtaagaatgctctg 699
DB 6137 AATTGAACATGATGCTTTCCAAAGGCTTAACCAAAACCAATGTACACAGGTATCGCTG 6078
XX
700 gttactcgagatggtgaaatggtgtgacgaagtgatgaacgcaatttgatcagcagatc 759
DB 6077 TTTACCAACAACGCTTACTTACGCTGACGCAATTCGCAAAAGTAATTAACGACGCTGCC 6018
XX
760 agtcacacacatgagcggatgaagtgatgctgtgagtgatcttcgtgtgatatcgtaag 819
DB 6017 GTGCTGCGAGTTTCTTAAAGAGTCCAGCTGTTGTAATTCACAGTAACCTCGGTTCC 5958
XX
820 aagacgcagtgatgaagtgatctatctcaatc 850
XXXXX

DB 5957 AAGAAATCGATGAAAGCTCATCTACGAGTTC 5927
RESULT 10
296319/c
ID 296319 standard; DNA: 2280 BP.
XX
XX 296319;
XX
XX 10-APR-2000 (first entry)
XX
DE S. pneumoniae derived DNA from ORF #147.
XX
XX Treatment; prevention; disease; diagnosis; gene therapy; screening;
XX bacterial; antimicrobial; antibiotic; pathogenesis; infection; ss.
XX Streptococcus pneumoniae.
XX
XX WO9806734-A1.
XX
XX 19-FEB-1998.
XX
XX 15-AUG-1997; 97WO-US1436.
XX
XX 16-AUG-1996; 96US-0024022.
XX
XX (SMIK) SMITHKLINE BEECHAM CORP.
XX
XX Black MT, Hodgson JE, Knowles DJC, Lonetto MA, Nicholas RO;
XX Stodola RK;
XX WPI: 1998-159452/14.
XX P-PSDB: Y85970.
XX
XX Streptococcus pneumoniae proteins and related DNA - useful for
XX screening compounds for antibacterial activity
XX
XX Claim 4; Page 180-181; 640pp; English.
XX
XX This invention describes novel isolated Streptococcus pneumoniae
XX polynucleotides (see 296319-296494) and their encoded proteins (see
XX Y85792-Y86182). The DNA, vectors and host cells described in the method
XX of the invention are useful for the recombinant expression of the
XX polypeptides. The polypeptides are useful for treatment or prevention of
XX disease, or diagnosis of disease related to expression or activity of
XX such a polypeptide. They can also be used to screen for compounds which
XX interact with and inhibit or activate such a polypeptide. The
XX polypeptides (or DNA encoding them, via gene therapy) are also useful
XX for inducing an immunological response in a mammal. The antagonists are
XX useful to inhibit such bacterial polypeptides. The polypeptides are
XX particularly useful to identify antimicrobial compounds and antibiotics.
XX They are also useful to determine their role in pathogenesis of
XX infection, dysfunction and disease.
XX
XX Sequence 2280 BP; 639 A; 524 C; 444 G; 673 T; 0 other;
Query Match 2.7%; Score 58.2; DB 19; Length 2280;
Best Local Similarity 46.0%; Pred. NO. 4.6e-08;
Matches 235; Conservative 0; Mismatches 273; Indels 3; Gaps 1;
XX
343 cagaacaattatgacacttggaaagctcaagtgatgaagcgaattatgtgtgctg 402
DB 945 CTGACGCAATGCTTAACTATTGAAACATGCGGCGTAGATACATCTACGATCCCAT 886
XX
403 gtgacagccctaatacgcgactgctgtccgcaaa---tcagatatgaagtgatgac 459
DB 885 CAGGAACCTCAGCTCATCTTGAATGACGCTTGGCTGAGACAAAGATATCCGTTCTTAC 826
XX
460 acgttcgaatgaaggaagcgcgcgttgcacgcgcgtgacgaatcgttgatcactggg 519
DB 825 AAGTTCCGCGACGAAAGACAGTGTCTTGGACGCGTTATGCAACGTAATTCGGCGCT 766
XXXXX

PD 25-AUG-1992.
 XX
 PF 26-AUG-1986; 86US-0900609.
 XX
 PR 26-AUG-1986; 86US-0900609.
 PR 04-MAR-1988; 88US-0164360.
 PR 18-JAN-1991; 91US-0642976.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 PI Bedbrook JR, Chaleff RS, Falco SC, Mazur BJ, Somerville CR;
 PI Yadav NS;
 XX
 DR WPI: 1992-307863/37.
 P-PSDB: R26912.
 XX
 PT Conferring herbicide resistance on plants - using a nucleic acid
 PT fragment encoding a herbicide-resistant plant aceto:lactate
 PT synthase protein
 XX
 PS Disclosure: Fig 5; 63pp; English.
 CC The DNA sequence is that of a mutant acetolactate synthetase gene
 CC isolated from herbicide-resistant strains of tobacco; and is
 CC designated the C3 mutant. The C3 mutant ALS gene may be isolated
 CC from plants resistant to sulphonylurea, triazopyrimidine
 CC sulphonamide and imidazolinone herbicides. The gene may be used to
 CC transform plants to confer herbicide resistance to plants such as
 CC tobacco, petunia, cotton, sugarbeet, potato, tomato, lettuce,
 CC sunflower, soybean, corn, wheat, rice, poplars, alfalfa, oats, etc.
 CC The herbicide resistant ALS genes can also be used as markers for
 CC transformation of an organism by a second DNA fragment.
 CC See also Q28387-9.
 XX
 SQ Sequence 2520 BP; 602 A; 565 C; 594 G; 759 T; 0 other;

 Query Match 2.6%; Score 55.2; DB 13; Length 2520;
 Best Local Similarity 49.7%; Pred. No. 4.5e-07;
 Matches 169; Conservative 0; Mismatches 168; Indels 3; Gaps 1;

 QY 1394 tttgctattacacctgaatcgttgcctctatttgaacagactggcgataagatgc 1453
 DB 1542 tgatgcaattccctccgcaatattgtctacaggttcagatgagtaactaatgggaatgc 1601
 QY 1454 ggtgttactgttgataccgcatgtgcaatgtgtgcatcgaggtacatcgagaatcc 1513
 DB 1602 tattataagtaactgtgtgtgggcaacacagatgtgtgctgtcctaatactataagtaacg 1661
 QY 1514 ggaaggaaacgcgactgtgtgtgtcattccgcacagcgacgactggttaattgcttgc 1573
 DB 1662 aaag---ccacgcacaaatgtgtgacatcgtgtgataagagacagtggaattgttgc 1718
 QY 1574 tcatcgatattgtgtgcgaagatgttatacgaacgcgcaggtgatacgtatgtgtgcga 1633
 DB 1719 cgtctgcatattgtgtgcgctgtgtggaacgcggaatgaattgtgtgtgatactatgtatga 1778
 QY 1634 tgggtgttgggacatgcatgctgtgaggttcttcgaccttgaacctcaccacaatttcgcgc 1693
 DB 1779 tggcagtttcatcatcgaatgaatgtgcaggaacttgcacaataaagtcggagaatctccacgt 1838
 QY 1694 gaaggctgtgtgttacaacagatctcttgggacatgtgtc 1733
 DB 1839 taagattatgttactgaataatcaacacacttgggaatgtgtc 1878

 RESUME 15
 Q81182
 ID Q81182 standard; DNA: 2520 BP.
 XX
 AC Q81182;
 XX
 DT 16-AUG-1995 (first entry)

XX
 DE ALS SUR4-C3 (P197E) mutant gene.
 XX
 KW Acetolactate-synthase: ALS; herbicide-resistance; tobacco;
 KW transgenic plant; crop improvement; chlorosulfuron;
 KW sulfometuron methyl; mutagenesis; SUR4-C3 gene; ss.
 XX
 OS Nicotiana tabacum var. xanthi.
 XX
 FH Key Location/Qualifiers
 FT CDS 175..2177
 FT /tag= a
 XX
 XX US5378824-A.
 XX
 PD 03-JAN-1995.
 PD
 XX 26-AUG-1986; 86US-0900609.
 PR 27-JUL-1987; 87IL-0083348.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 PI Bedbrook JR, Chaleff RS, Falco SC, Mazur BJ, Somerville CR;
 PI Yadav NS;
 XX
 DR WPI: 1995-065894/09.
 DR P-PSDB: R63081.
 XX
 PT Nucleic acid fragment encoding a plant aceto:lactate synthase -
 PT confers herbicide resistance when introduced to
 PT herbicide-sensitive plants
 XX
 PS Disclosure: Fig. 5A-5D; 62pp; English.
 CC Callus cultures of herbicide-sensitive tobacco var. xanthi were
 CC exposed to sulfometuron methyl (SM) at 2 ppb. Resistant cell lines
 CC C3 and S4 were selected. The acetolactate-synthase (ALS) of
 CC C3 cells showed 100-fold more resistance to chlorosulfuron and SM
 CC than the wild-type enzyme resulting from a P197E mutation in the
 CC SUR4 gene.
 XX
 SQ Sequence 2520 BP; 602 A; 565 C; 594 G; 759 T; 0 other;

 Query Match 2.6%; Score 55.2; DB 16; Length 2520;
 Best Local Similarity 49.7%; Pred. No. 4.5e-07;
 Matches 169; Conservative 0; Mismatches 168; Indels 3; Gaps 1;

 QY 1394 tttgctattacacctgaatcgttgcctctatttgaacagactggcgataagatgc 1453
 DB 1542 tgatgcaattccctccgcaatattgtctacaggttcagatgagtaactaatgggaatgc 1601
 QY 1454 ggtgttactgttgataccgcatgtgcaatgtgtgcatcgaggtacatcgagaatcc 1513
 DB 1602 tattataagtaactgtgtgtgggcaacacagatgtgtgctgtcctaatactataagtaacg 1661
 QY 1574 tcatcgatattgtgtgcgaagatgttatacgaacgcgcaggtgatacgtatgtgtgcga 1633
 DB 1719 cgtctgcatattgtgtgcgctgtgtggaacgcggaatgaattgtgtgtgatactatgtatga 1778
 QY 1634 tgggtgttgggacatgcatgctgtgaggttcttcgaccttgaacctcaccacaatttcgcgc 1693
 DB 1779 tggcagtttcatcatcgaatgaatgtgcaggaacttgcacaataaagtcggagaatctccacgt 1838
 QY 1694 gaaggctgtgtgttacaacagatctcttgggacatgtgtc 1733
 DB 1839 taagattatgttactgaataatcaacacacttgggaatgtgtc 1878

BEST AVAILABLE COPY

BEST AVAILABLE COPY

BEST AVAILABLE COPY